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1102

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,545

DATE: 01/14/2002

TIME: 10:30:36

Input Set : N:\Crf3\RULE60\09966545.raw

Output Set: N:\CRF3\01142002\I966545.raw

1 <110> APPLICANT: Fernandes, Elma
 2 Vernet, Corine
 3 Shimkets, Richard A.
 4 <120> TITLE OF INVENTION: Novel Human Proteins and Polynucleotides Encoding
 5 Them
 6 <130> FILE REFERENCE: Cura-46 (15966-546)
 7 <140> CURRENT APPLICATION NUMBER: US/09/966,545
 8 <141> CURRENT FILING DATE: 2001-09-26
 9 <150> PRIOR APPLICATION NUMBER: 09/544,511
 10 <151> PRIOR FILING DATE: 2000-04-06
 11 <160> NUMBER OF SEQ ID NOS: 57
 12 <170> SOFTWARE: PatentIn Ver. 2.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 1107
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (65)..(598)
 21 <400> SEQUENCE: 1

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 23 cgga atg gac tgg cct cac aac ctg ctg ttt ctt ctt acc att tcc atc 109
 24 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
 25 1 5 10 15
 26 ttc ctg ggg ctg ggc agc cag gag ccc caa aag caa gag gaa ggg gca 157
 27 Phe Leu Gly Leu Gly Ser Gln Glu Pro Gln Lys Gln Glu Glu Ala
 28 20 25 30
 29 agg gcg gcc tgg gcc ctg gcc tgg cct cac cag gtg cca ctg gac ctg 205
 30 Arg Ala Ala Trp Ala Leu Ala Trp Pro His Gln Val Pro Leu Asp Leu
 31 35 40 45
 32 gtg tca cgg atg aaa ccg tat gcc cgc atg gag gag tat gag agg aac 253
 33 Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn
 34 50 55 60
 35 atc gag gag atg gtg gcc cag ctg agg aac agc tca gag ctg gcc cag 301
 36 Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln
 37 65 70 75
 38 aga aag tgt gag gtc aac ttg cag ctg tgg atg tcc aac aag agg agc 349
 39 Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser
 40 80 85 90 95
 41 ctg tct ccc tgg ggc tac agc atc aac cac gac ccc agc cgt atc ccc 397
 42 Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro
 43 100 105 110
 44 gtg gac ctg ccg gag gca cgg tgc ctg tgt ctg ggc tgt gtg aac ccc 445
 45 Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro
 46 115 120 125
 47 ttc acc atg cag gag gac cgc agc atg gtg agc gtg ccg gtg ttc agc 493
 48 Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser

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51  Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly
52          145          150          155
53  cct tgc cgc cag cgc gca gtc atg gag acc atc gct gtg ggc tgc acc 589
54  Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr
55  160          165          170          175
56  tgc atc ttc tgaatcacct ggcccagaag ccaggccagc agcccagac 638
57  Cys Ile Phe
58  catcctcctt gcacctttgt gccaagaaag gcctatgaaa agtaaact gacttttgaa 698
59  agcaaaaaaa ccccaggaag cttcggtctg gttccagaca catggaaaac agacttcctg 758
60  tgccagcgca tgctgatccc ttcagcagcc gcttctccac ccttggggct gctctccagc 818
61  acctggcagt gtccagagcg gataggggcg ccgtgtttgg tgaatgagtg cacagacgcc 878
62  tctaggggga gcccaagatc tgctcctgc ctccctctat tatgccttca taggtgggtc 938
63  agaacaaaga attccttacc aacctcccg gtccccact gccaatcacc cacctccatt 998
64  ctaccctcta cagctgcccc ttatccccca aagtcctgaa attttgcttg ggtcacctgc 1058
65  tccaggaggc agagttccca tgaagggtat taaacgtcta ctacactgc 1107
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68 <211> LENGTH: 178
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
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73    1          5          10          15
74  Leu Gly Leu Gly Ser Gln Glu Pro Gln Lys Gln Glu Glu Gly Ala Arg
75          20          25          30
76  Ala Ala Trp Ala Leu Ala Trp Pro His Gln Val Pro Leu Asp Leu Val
77          35          40          45
78  Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile
79          50          55          60
80  Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg
81          65          70          75          80
82  Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu
83          85          90          95
84  Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val
85          100          105          110
86  Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe
87          115          120          125
88  Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln
89          130          135          140
90  Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro
91          145          150          155          160
92  Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys
93          165          170          175
94  Ile Phe
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 1603
98 <212> TYPE: DNA
99 <213> ORGANISM: Homo sapiens

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102 <222> LOCATION: (92)..(1123)
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105      aaaaagaaga aaaagaagaa gaaaaaaaat c atg aaa acc atc cag cca aaa 112
106                      Met Lys Thr Ile Gln Pro Lys
107                      1                      5
108      atg cac aat tct atc tct tgg gca atc ttc acg ggg ctg gct gct ctg 160
109      Met His Asn Ser Ile Ser Trp Ala Ile Phe Thr Gly Leu Ala Ala Leu
110                      10                      15                      20
111      tgt ctc ttc caa gga gtg ccc gtg cgc agc gga gat gcc acc ttc ccc 208
112      Cys Leu Phe Gln Gly Val Pro Val Arg Ser Gly Asp Ala Thr Phe Pro
113                      25                      30                      35
114      aaa gct atg gac aac gtg acg gtc cgg cag ggg gag agc gcc acc ctc 256
115      Lys Ala Met Asp Asn Val Thr Val Arg Gln Gly Glu Ser Ala Thr Leu
116      40                      45                      50                      55
117      agg tgc act att gac aac cgg gtc acc cgg gtg gcc tgg cta aac cgc 304
118      Arg Cys Thr Ile Asp Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg
119                      60                      65                      70
120      agc acc atc ctc tat gct ggg aat gac aag tgg tgc ctg gat cct cgc 352
121      Ser Thr Ile Leu Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg
122                      75                      80                      85
123      gtg gtc ctt ctg agc aac acc caa acg cag tac agc atc gag atc cag 400
124      Val Val Leu Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln
125                      90                      95                      100
126      aac gtg gat gtg tat gac gag ggc cct tac acc tgc tgc gtg cag aca 448
127      Asn Val Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr
128      105                      110                      115
129      gac aac cac cca aag acc tct agg gtc cac ctc att gtg caa gta tct 496
130      Asp Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
131      120                      125                      130                      135
132      ccc aaa att gta gag att tct tca gat atc tcc att aat gaa ggg aac 544
133      Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly Asn
134                      140                      145                      150
135      aat att agc ctc acc tgc ata gca act ggt aga cca gag cct acg gtt 592
136      Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro Thr Val
137      155                      160                      165
138      act tgg aga cac atc tct ccc aaa gcg gtt ggc ttt gtg agt gaa gac 640
139      Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val Ser Glu Asp
140      170                      175                      180
141      gaa tac ttg gaa att cag ggc atc acc cgg gag cag tca ggg gac tac 688
142      Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln Ser Gly Asp Tyr
143      185                      190                      195
144      gag tgc agt gcc tcc aat gac gtg gcc gcg ccc gtg gta cgg aga gta 736
145      Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro Val Val Arg Arg Val
146      200                      205                      210                      215
147      aag gtc acc gtg aac tat cca cca tac att tca gaa gcc aag ggt aca 784
148      Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile Ser Glu Ala Lys Gly Thr

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150  ggt gtc ccc gtg gga caa aag ggg aca ctg cag tgt gaa gcc tca gca 832
151  Gly Val Pro Val Gly Gln Lys Gly Thr Leu Gln Cys Glu Ala Ser Ala
152          235          240          245
153  gtc ccc tca gca gaa ttc cag tgg tac aag gat gac aaa aga ctg att 880
154  Val Pro Ser Ala Glu Phe Gln Trp Tyr Lys Asp Asp Lys Arg Leu Ile
155          250          255          260
156  gaa gga aag aaa ggg gtg aaa gtg gaa aac aga cct ttc ctc tca aaa 928
157  Glu Gly Lys Lys Gly Val Lys Val Glu Asn Arg Pro Phe Leu Ser Lys
158          265          270          275
159  ctc atc ttc ttc aat gtc tct gaa cat gac tat ggg aac tac act tgc 976
160  Leu Ile Phe Phe Asn Val Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys
161          280          285          290          295
162  gtg gcc tcc aac aag ctg ggc cac acc aat gcc agc atc atg cta ttt 1024
163  Val Ala Ser Asn Lys Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe
164          300          305          310
165  ggt cca ggc gcc gtc agc gag gtg agc aac ggc acg tcg agg agg gca 1072
166  Gly Pro Gly Ala Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala
167          315          320          325
168  ggc tgc gtc tgg ctg ccg cct ctt ctg gtc ttg cac ctg ctt ctc aaa 1120
169  Gly Cys Val Trp Leu Pro Pro Leu Leu Val Leu His Leu Leu Leu Lys
170          330          335          340
171  ttt tgatgtgagt gccacttccc caccgaggaa aggctgccgc caccaccacc 1173
172  Phe
173  accaacacaa cagcaatggc aacaccgaca gcaaccaatc agatatatac aaatgaaatt 1233
174  agaagaaaca cagcctcatg ggacagaaat ttgagggagg ggaacaaaga atactttggg 1293
175  gggaaaagag ttttaaaaaa gaaattgaaa attgccttgc agatatattag gtacaatgga 1353
176  gttttctttt cccaaacggg aagaacacag cacaccggc ttggaccac tgcaagctgc 1413
177  atcgtgcaac ctctttggtg ccagtgtggg caagggtcca gcctctctgc ccacagagtgc 1473
178  cccccacgtg gaacattctg gagctggcca tcccaaattc aatcagtcga tagagacgaa 1533
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184 <212> TYPE: PRT
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190          20          25          30
191  Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val Thr Val Arg
192          35          40          45
193  Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp Asn Arg Val Thr
194          50          55          60
195  Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp
196          65          70          75          80
197  Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr
198          85          90          95

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199   Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro
200               100               105               110
201   Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
202               115               120               125
203   His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
204               130               135               140
205   Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
206   145               150               155               160
207   Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
208               165               170               175
209   Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr
210               180               185               190
211   Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala
212               195               200               205
213   Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
214   210               215               220
215   Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
216   225               230               235               240
217   Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr
218               245               250               255
219   Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu
220               260               265               270
221   Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His
222               275               280               285
223   Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr
224   290               295               300
225   Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser
226   305               310               315               320
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242   gctcctgtct cttaaatcag ctagcctgat ttgccagta aatgattcct gagagtgtgt 180
243   gtgcgtgtgt gtgtgtgtgt gtgcccgcgc gcgtgtgttg tagctctgtc aatccttgga 240
244   ttagaaccaa tgattgcagc ttgtaagagg gctgtccagg gccagattgt acaatgtgtc 300
245   tcagtgccag agtatgagtg gagataatta cggagaagtc atactctctc acaccctcgg 360
246   ctttcttggt gtgtccttca gcaaaacagt ggattttaat ctcttgacac aagcttgaga 420
247   gcaacacaat ctatcaggaa agaaagaaag aaaaaaacccg aacctgacaa aaaagaagaa 480
248   aaagaagaag aaaaaaaatc atg aaa acc atc cag cca aaa atg cac aat tct 532

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\01142002\I966545.raw

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